IN THE SPECIFICATION

At page 18, please replace paragraph [0067] with the following text:

For general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al. (1997, Protein 28:405-420) and ~~http://~~www.psc.edu/general/ software/packages/pfam/pfam.html.

At page 19, please replace paragraphs [0069]-[0070] with the following text:

A 69087 polypeptide can include a pkinase domain. As used herein, the term "pkinase domain" refers to a protein domain having an amino acid sequence of about 200-300 amino acid residues in length, preferably, at least about 225-300 amino acids, more preferably about 278 amino acid residues or about 251 amino acid residues and has a bit score for the alignment of the sequence to the pkinase domain (HMM) of at least 100 or greater, preferably 200 or greater, and more preferably 300 or greater. The pkinase domain has been assigned the PFAM accession PF00069 (~~http://~~genome.wustl.edu/Pfam/html).

A 69087 polypeptide can also include one or more Regulator of G protein Signaling (RGS) domains. As used herein, the term "RGS domain" refers to a protein domain having a conserved amino acid sequence as described (Watson et al., 1996, Nature 383:172-175 and references cited therein). The RGS domain has been assigned the PFAM accession PF00615 (~~http://~~genome.wustl.edu/Pfam/html).

At pages 19-20, please replace paragraph [0072] with the following text:

To identify the presence of a pkinase domain profile in a 69087 receptor, the amino acid sequence of the protein is searched against a database of HMMs (e.g., the Pfam database, release 2.1) using common default parameters (~~http://~~www.sanger.ac.uk/Software/Pfam/HMM_search). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for PF00069 and score of 100 is the default threshold score for determining a hit. For example, using ORFAnalyzer software, a pkinase domain profile was identified in the amino acid sequence of SEQ ID NO: 2 (e.g., amino acids 53-303 of SEQ ID NO: 2). Accordingly, a 69087 protein having at least about 60-70%, more preferably about 70-80%, or about 80-90% homology with the

pkinase domain profile of human 69087 is within the scope of the invention. To identify the presence of an RGS domain profile in a 69087 receptor, the amino acid sequence of the protein is searched using a family specific default program for PF00615 and a default score of 1 or greater (preferably 10 or greater).

At page 24, please replace paragraph [0085] with the following text:

For general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al. (1997, Protein 28:405-420) and ~~http:~~//www.psc.edu/general/ software/packages/pfam/pfam.html.

At pages 24-25, please replace paragraph [0087] with the following text:

A 15821 polypeptide can include a C3HC4 type zing finger domain (a RING finger domain). As used herein, the term "RING finger domain" refers to a protein domain having an amino acid sequence of about 30-70 amino acid residues in length, preferably, at least about 40-70 amino acids, more preferably about 46 amino acid residues and has a bit score for the alignment of the sequence to the RING finger domain (HMM) of at least 5 or greater, preferably 10 or greater, and more preferably 13 or greater. The RING finger domain has been assigned the PFAM accession PF00097 (~~http:~~//genome.wustl.edu/Pfam/html).

At pages 25-26, please replace paragraphs [0089]-[0090] with the following text:

To identify the presence of a RING finger domain profile in a 15821 receptor, the amino acid sequence of the protein is searched against a database of HMMs (e.g., the Pfam database, release 2.1) using common default parameters such as those found at (~~http:~~//www.sanger.ac.uk/Software/Pfam/HMM_search). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for PF00097 and score of 5 is the default threshold score for determining a hit. For example, using ORFAnalyzer software, a RING finger domain profile was identified in the amino acid sequence of SEQ ID NO: 22 (e.g., amino acids 483-528 of SEQ ID NO: 22). Accordingly, a 15821 protein having at least about 60-70%, more preferably about 70-80%, or about 80-90% homology with the RING finger domain profile of human 15821 is within the scope of the invention.

In one embodiment, a 15821 protein includes at least one transmembrane domain. As used herein, the term "transmembrane domain" includes an amino acid sequence of about 5 amino acid residues in length that spans the plasma membrane. More preferably, a transmembrane domain includes about at least 10, 15, 20 or 22 amino acid residues and spans a membrane. Transmembrane domains are rich in hydrophobic residues, and typically have an alpha-helical structure. In a preferred embodiment, at least 50%, 60%, 70%, 80%, 90%, or 95% or more of the amino acids of a transmembrane domain are hydrophobic, e.g., leucines, isoleucines, tyrosines, or tryptophans. Transmembrane domains are described in, for example, ~~htto://~~pfam.wustl.edu/cgi-bin/getdesc?name=7tm-1, and Zagotta W.N. et al. (1996, Annu. Rev. Neurosci. 19: 235-263), the contents of which are incorporated herein by reference. Amino acid residues 470 to about 482 of SEQ ID NO: 22 comprise a transmembrane domain in a 15821 protein. In one embodiment, the amino-terminal domain of 15821 protein (i.e., about residues 1-469 of SEQ ID NO: 22) is on the cytoplasmic side of a cellular membrane (e.g., the nuclear membrane or the cytoplasmic membrane) and the carboxyl-terminal domain (i.e., about residues 483-564 of SEQ ID NO: 22) is on the non-cytoplasmic side of the same membrane. In another embodiment, the amino-terminal domain is oriented on the non-cytoplasmic side of the membrane and the carboxyl-terminal domain is oriented on the cytoplasmic side.

At page 30, please replace paragraph [0105] with the following text:

For general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al. (1997, Protein 28:405-420) and ~~http://~~www.psc.edu/general/ software/packages/pfam/pfam.html.

At page 30, please replace paragraph [0107] with the following text:

A 15418 polypeptide can include a dual specificity phosphatase catalytic domain (DSPc) domain. As used herein, the term " DSPc domain" refers to a protein domain having an amino acid sequence of about 100-300 amino acid residues in length, preferably, at least about 125-300 amino acids, more preferably about 138 amino acid residues and has a bit score for the alignment of the sequence to the DSPc domain (HMM) of at least 50 or greater, preferably 100 or greater, and more preferably 125 or greater. The DSPc domain has been assigned the PFAM accession PS50054 (~~http://~~genome.wustl.edu/Pfam/html).

At page 31, please replace paragraph [0109] with the following text:

To identify the presence of a DSPc domain profile in a 15418 receptor, the amino acid sequence of the protein is searched against a database of HMMs (e.g., the Pfam database, release 2.1) using common default parameters such as those found at (~~http://~~www.sanger.ac.uk/Software/Pfam/HMM_search). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for PS50054 and score of 50 is the default threshold score for determining a hit. For example, using ORFAnalyzer software, a DSPc domain profile was identified in the amino acid sequence of SEQ ID NO: 42 (e.g., amino acids 21-159 of SEQ ID NO: 42). Accordingly, a 15418 protein having at least about 60-70%, more preferably about 70-80%, or about 80-90% homology with the DSPc domain profile of human 15418 is within the scope of the invention.

At pages 41-42, please replace paragraph [0141] with the following text:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman et al. (1970, J. Mol. Biol. 48:444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at ~~http://~~www.gcg.com), using either a BLOSUM 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at ~~http://~~www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within a sequence identity or homology limitation of the invention) are a BLOSUM 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

At page 142, please replace paragraph [0143] with the following text:

The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related

sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990, J. Mol. Biol. 215:403-410). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 69087, 15821, or 15418 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to 69087, 15821, or 15418 protein molecules of the invention. To obtain gapped alignments for comparison purposes, gapped BLAST can be utilized as described in Altschul et al. (1997, Nucl. Acids Res. 25:3389-3402). When using BLAST and gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <~~http://~~www.ncbi.nlm.nih.gov>.